This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1–54. (Canceled)

55. (currently amended) An isolated polynucleotide encoding an intact antibody comprising a variant heavy chain wherein the variant heavy chain comprises a variant hinge region which does not form inter-heavy chain disulfide linkages, and wherein said variant hinge region lacks a cysteine residue, wherein the cysteine residue forms an inter-chain disulfide linkage when present.

56.-57. (Cancelled)

58. (currently amended) A recombinant vector comprising the polynucleotide ~~for expressing the antibody~~ of claim 55.

59. (Previously presented) A prokaryotic host cell comprising the recombinant vector of claim 58.

60. (Original) The host cell of claim 59 which is a prokaryotic cell.

61. (Original) The host cell of claim 60 which is a gram-negative bacterial cell.

62. (Original) The host cell of claim 61 which is E. coli.

63. (Currently Amended) The host cell of claim 62, further comprising a polynucleotide encoding at least one prokaryotic polypeptide selected from the group consisting of disulfide bond A (DsbA), disulfide bond C (DsbC), disulfide bond G

(DsbG) and FkpA.

64. (Currently Amended) The host cell of claim 63, wherein the polynucleotide encodes both disulfide bond A (DsbA) and disulfide bond C (DsbC).

65. (Previously presented) The host cell of claim 62, wherein the E. coli is of a strain deficient in endogenous protease activities.

66. (Previously presented) A method of producing an intact antibody comprising expressing in a prokaryotic host cell the polynucleotide of claim 55, wherein the amount of intact antibody produced from the host cell is increased in comparison to the amount of aggregated heavy chain produced in the host cell, and recovering said intact antibody from the host cell.

67. (Previously presented) The method of claim 66, wherein at least two inter-heavy chain disulfide linkages of the antibody are eliminated.

68. (Previously presented) The method of claim 66, wherein all inter-heavy chain disulfide linkages of the antibody are eliminated.

69. (cancelled)

70. (currently amended) The method of claim 66 ~~69~~, wherein said variant hinge region lacks at least two of the cysteine residues, wherein each of the at least two cysteine residues form an inter-chain disulfide linkage when present.

71. (currently amended) The method of claim 66-~~69,~~ wherein said variant hinge region lacks all of the cysteine residues, wherein all of the cysteine residues form an inter-chain disulfide linkage when present.

72. (currently amended)The method of claim 66 ~~69~~, wherein a cysteine of the hinge region is deleted or substituted with another amino acid.

73. (Original) The method of claim 72, wherein said cysteine residue is substituted with serine.

74. (Previously presented) The method of claim 66, wherein said antibody is a full-length antibody.

75. (Previously presented) The method of claim 66, wherein said antibody is humanized.

76. (Previously presented) The method of claim 66, wherein said antibody is human.

77. (Previously presented) The method of claim 66, wherein said antibody is an antibody fragment.

78. (Original) The method of claim 77, wherein said antibody fragment is an Fc fusion polypeptide.

79. (Previously presented) The method of claim 66, wherein said antibody comprises a heavy chain constant domain and a light chain constant domain.

80. (Previously presented) The method of claim 66, wherein said antibody is selected from the group consisting of IgG, IgA and IgD.

81. (Previously presented) The method of claim 66, wherein said antibody is selected from the group consisting of IgG, IgA, IgE, IgM and IgD.

82. (Previously presented) The method of claim 80, wherein the antibody is IgG.

83. (Previously presented) The method of claim 82, where said antibody is IgGl or IgG2.

84. (Previously presented) The method of claim 66, wherein said antibody is selected from the group consisting of therapeutic, agonist, antagonist, diagnostic, blocking and neutralizing antibodies.

85. (Original) The method of claim 66, wherein heavy and light chains of said antibody are encoded by a single polynucleotide.

86. (Withdrawn) The method of claim 66, wherein heavy and light chains of said antibody are encoded by separate polynucleotides.

87. (Previously presented) The method of claim 66, further comprising determining that the antibody that is recovered is biologically active.

88. (Previously presented) The method of claim 66, wherein the amount of said antibody produced is at least about 10% greater than the amount of a reference antibody expressed under similar conditions, wherein said reference antibody has a wild type ability to form disulfide linkages.

89. (Previously presented) The method of claim 88, wherein said antibody comprises a variant immunoglobulin heavy chain hinge region lacking at least one cysteine residue wherein the at least one cysteine residue forms an inter-chain disulfide linkage when present, and wherein said reference antibody comprises an immunoglobulin heavy chain hinge region that is the wild type counterpart of the hinge region of the antibody.

90. (Previously presented) The method of claim 88, wherein the amount is at least about 25%.

91. (Previously presented) The method of claim 90, wherein the amount is at least about 50%.

92. (Previously presented) The method of claim 91, wherein the amount is at least about 75%.

93. (Previously presented) The method of claim 66, wherein the antibody and reference antibody have substantially similar antigen binding capabilities.

94. (Previously presented) The method of claim 66, wherein the antibody and reference antibody have substantially similar FcRn binding capabilities.

95. (Previously presented) The method of claim 66, wherein the antibody and reference antibody have substantially similar pharmacokinetic values.

96. (Previously presented) The method of claim 66, wherein said host cell is prokaryotic.

97. (Previously presented) The method of claim 96, wherein said host cell is a gram-negative bacterial cell.

98. (Previously presented) The method of claim 97, wherein said host cell is E. coli.

99. (Currently Amended) The method of claim 96, further comprising expressing in the host cell a polynucleotide encoding at least one prokaryotic polypeptide selected from

the group consisting of disulfide bond A (DsbA), disulfide bond C (DsbC), disulfide bond G (DsbG) and FkpA.

100. (Previously presented) The method of claim 99, wherein the polynucleotide encodes both DsbA and DsbC.

101. (Previously presented) The method of claim 98, wherein the E. coli is of a strain deficient in endogenous protease activities.

102. (Cancelled)

103. (Previously presented) The method of claim 66, wherein said antibody is recovered from cell lysate.

104. (Previously presented) The method of claim 66, wherein said antibody is recovered from culture medium or the periplasm.

105. (currently amended) A method for producing an intact antibody comprising: expressing in a prokaryotic host cell a polynucleotide encoding a variant immunoglobulin heavy chain; wherein said variant immunoglobulin heavy chain comprises a hinge region in which at least one cysteine is modified, wherein the at least one cysteine residue forms an inter-chain disulfide linkage when present and when modified no longer forms a disulfide linkage, and wherein said variant immunoglobulin heavy chain comprises a reduced ability to form a disulfide linkage such that amount of self aggregation of the variant immunoglobulin heavy chain is less than the amount of self aggregation of a reference immunoglobulin heavy chain when expressed under similar conditions,

wherein the reference immunoglobulin heavy chain has a wild type ability to form a disulfide linkage.

106. (cancelled)

107. (currently amended)The method of claim 105 ~~106,~~ wherein at least two cysteines are modified.

108. (currently amended)The method of claim 105 ~~106~~, wherein all cysteines are modified.

109. (currently amended)The method of claim 105 ~~106,~~ wherein said cysteine when present forms an intermolecular disulfide linkage.

110. (currently amended)The method of claim 105 ~~106,~~ wherein the amount of aggregation of the variant heavy chain is at least about 10% less than the amount of self aggregation of the reference immunoglobulin heavy chain.

111. (Original) The method of claim 110, wherein the amount of aggregation of the variant heavy chain is at least about 25% less than the amount of self aggregation of the reference immunoglobulin heavy chain.

112. (Original) The method of claim 111, wherein the amount of aggregation of the variant heavy chain is at least about 50% less than the amount of aggregation of the reference immunoglobulin heavy chain.

113. (Previously presented) The method of claim 112, wherein the amount of aggregation of the variant heavy chain is at least about 75% less than the amount of self aggregation of the reference immunoglobulin heavy chain.

114. (Cancelled)

115–120. (Cancelled)

121. (new) A method for decreasing aggregation of an immunoglobulin heavy chain comprising: expressing in a host cell a polynucleotide encoding a variant immunoglobulin heavy chain; wherein said variant immunoglobulin heavy chain comprises a hinge region in which at least one cysteine is modified, wherein the at least one cysteine residue forms an inter-chain disulfide linkage when present and when modified no longer forms a disulfide linkage, and wherein said variant immunoglobulin heavy chain comprises a reduced ability to form a disulfide linkage such that amount of self aggregation of the variant immunoglobulin heavy chain is less than the amount of self aggregation of a reference immunoglobulin heavy chain when expressed under similar conditions,

wherein the reference immunoglobulin heavy chain has a wild type ability to form a disulfide linkage.

122. (new)The method of claim 121, wherein at least two cysteines are modified.

123. (new)The method of claim 121, wherein all cysteines are modified.

124. (new)The method of claim 123, wherein the modification is the substitution of the cysteines with serine.

125. (new)The method of claim 121, wherein the amount of aggregation of the variant heavy chain is at least about 10% less than the amount of self aggregation of the reference immunoglobulin heavy chain.

126. (new) The method of claim 121, wherein the amount of aggregation of the variant heavy chain is at least about 25% less than the amount of self aggregation of the

reference immunoglobulin heavy chain.

127. (new) The method of claim 121 wherein the amount of aggregation of the variant heavy chain is at least about 50% less than the amount of aggregation of the reference immunoglobulin heavy chain.

128. (new) The method of claim 121, wherein the amount of aggregation of the variant heavy chain is at least about 75% less than the amount of self aggregation of the reference immunoglobulin heavy chain.

129. (new) The method of claim 121, wherein the host cell is prokaryotic.

130. (new) The method of claim 121, wherein the host cell is eukaryotic.

131. (new) The isolated polynucleotide of claim 55 further comprising a prokaryotic promoter.

132. (new) The isolated polynucleotide of claim 131 further comprising a secretion signal sequence.